Amendments to the Drawings:

Please replace the two drawing sheets comprising Figures 3 and 4, respectively, with the two attached replacement drawing sheets comprising Figures 3A and 4A.

Attachment: Two replacement sheets

REMARKS

Claims 82, 85 and 90 have been clarified as discussed below.

New claims 95-135 have been copied for purposes of preserving rights under 35 USC 135 b(1) and b(2). These claims will be discussed in more detail following the response to the office action below.

Response to Interview Summary

The 35 USC 112, second paragraph rejection of the phrase "the different probes in the first probe set have at least three interrogation positions respectively corresponding to each of at least three contiguous nucleotides in the reference sequence" was discussed. Applicants maintain the phrase is clear. Nevertheless alternative language was agreed with the Examiners as stated in the Examiners' interview summary. The claims have been amended to include this language. This amendment is made only for purposes of expediting allowance reserve the right to reinstate the original language for purposes of appeal should this goal not be achieved.

Drawings

The drawing sheets comprising FIGS 3 and 4 have been amended in accordance with 37 C.F.R. § 1.84, to relabel those figures as FIGS 3A and 4A, respectively. As the amendments to the drawings are limited to the relabeling of the figures, these amendments are not new matter. The specification also been amended to conform to the correctly labeled drawings. These amendment to the specification are also not new matter.

Abstract

Applicants provide a new abstract on a separate sheet.

Rejection under 35 USC 112, second paragraph

Applicants have amended claims 82, 85 and 90 using the agreed phrase from the Examiner's interview summary sheet. This amendment does not represent acquiescence in the PTO's position. Applicants maintain the previous claims were clear as is, and that the term "collectively" used previously is implicit in the disclosure.

Claim 90 also stands rejected for lack of antecedent basis for the term "segment." Segment has been replaced by "probe," which has antecedent basis.

Other matters

New claims 95-133 have been presented above for purposes of interference with U.S. Patent 6,881,571. New claims 95-110 and 133 represent modified versions of claims 1-7, 12, 13, 15-18 and 20-22 of U.S. 6,881,571, all of which are directed to devices for detecting at least one differentially spliced gene product and methods for making the same. The modifications which have been made in copying the patent claims are not substantive and are only made to accommodate for the use of different but equivalent terms in the disclosures.

Claims 95-132 find support in the specification as shown in the attached chart entitled "Representative Support for Applicants' Claims 95-132," it being understood that the references to the Applicants' disclosure there given are illustrative only and not intended to be all-inclusive.

No prohibited new matter has been added by way of these amendments.

It is noted that these claims are being filed prior to one year from the date on which U.S. 6,881,571 was granted (April 19, 2005), thereby satisfying the requirements of 35 U.S.C. §135(b)(1). In addition, the present application was filed prior to the publication dates for U.S. 20030165931 (published Sept. 4, 2003) and U.S. 0040191828 (published Sept. 30, 2004), each of which is related to U.S. 6,881,571. Accordingly, the requirements of 35 U.S.C. §135(b)(2) are also satisfied.

REPRESENTATIVE SUPPORT FOR APPLICANTS' CLAIMS 95-132

Claims 95-133	Exemplary Support in Specification
95. A device for detecting at least one variation in the splicing of a gene comprising	page 63, lines 23-37
an array of nucleic acid probes immobilized on a solid support, the array comprising at least two sets of probes of between 3 and 100 nucleotides in length,	page 2, lines 37-38 page 20, lines 33-36
wherein said array comprises at least a first and a second probe on the solid support,	page 68, lines 30-33; Fig. 10; page 81, lines 19-34
wherein said first probe comprises a first sequence that is complementary to an exon or an intron of a gene, and wherein said sequence corresponds to at least one region of variation corresponding to a splice sequence, and	page 14, lines 10-20; page 16, lines 33-36 page 63, lines 23-37
wherein said second probe comprises a second sequence that is complementary to an exon-intron boundary of said gene, and wherein said second sequence corresponds to at least one region of variation corresponding to a splice sequence,	page 4, lines 7-22 page 63, lines 15-17; page 70, line 31 to page 71, line 11
said device allowing, when hybridized with a target sequence, detection of the presence or absence of said at least one variation in the splicing of a gene.	page 63, lines 23-37 page 14, lines 15-34
96. The device of claim 95, wherein said probe sequences are publicly available.	page 63, lines 15-21
97. The device of claim 95, wherein the probes are immobilized on a chip.	page 2, lines 25-29

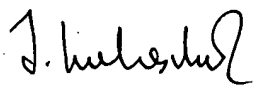
98. The device of claim 95, wherein said probes are oligodeoxyribonucleotides or oligoribonucleotides.	page 19, lines 29-32
99. The device of claim 95, wherein said probes comprise sequences of between 3 and 50 nucleotides.	page 20, lines 33-36
100. The device of claim 95, wherein said first and second probes exhibit complementarity to reference sequences comprising mutations or polymorphisms associated with phenotypic changes having clinical significance in human patients.	page 15, line 3 to page 16, line 32
101. The device of claim 100, wherein said first and second probes exhibit complementarity to reference sequences comprising mutations or polymorphisms associated with cancer.	page 15, line 17
102. A method of producing a device comprising an array of nucleic acid probes immobilized on a solid support, the array comprising at least two sets of probes of between 3 and 100 nucleotides in length, (a) providing said nucleic acid probes, wherein said probes comprise at least a first and a second probe, wherein said first probe comprises a first sequence that is complementary to an exon or an intron of a gene, and wherein said sequence corresponds to at least one region of variation corresponding to a splice sequence, and wherein said second probe comprises a second sequence that is complementary to an exon-intron boundary of said gene, and wherein said second sequence corresponds to at least one region of variation corresponding to a splice sequence; and (b) arranging and	page 2, lines 11-19; see support for claim 95

immobilizing said first and second probes adjacent to one another on the solid support, said device allowing, when hybridized with a target sequence, detection of the presence or absence of said at least one variation in the splicing of a gene.	
103. The method of claim 102, wherein said first or second probe is obtained by: (a) identifying at least two nucleic acid sequences corresponding to a splice sequence and a mutation in a splice sequence, respectively, wherein said mutation has a phenotypic effect of clinical significance, and (b) synthesizing nucleic acid probes containing complementarity to said splice sequence.	page 63, lines 23-25; page 15, line 3 to page 16, line 32
104. The method of claim 102, wherein said probe sequences are publicly available.	page 63, lines 15-21
105. The method of claim 102, wherein the probes are immobilized on a chip.	page 2, lines 25-29
106. The method of claim 102, wherein said first and second probes exhibit complementarity to reference sequences comprising mutations or polymorphisms associated with phenotypic changes having clinical significance in human patients.	page 15, line 3 to page 16, line 32
107. The method of claim 106, wherein said first and second probes exhibit complementarity to reference sequences comprising mutations or polymorphisms associated with cancer.	page 15, line 17
108. The method of claim 102, wherein said probes comprise sequences of between 3 and 50 nucleotides.	page 20, lines 33-36
109. The device of claim	page 62, lines 19-20

95, wherein said device allows detection of the presence or absence of said at least one variation in the splicing of a gene in an mRNA population.	
110. The device of claim 95, wherein said device allows detection of the presence or absence of at least one variation in the splicing of more than one gene.	page 27, lines 3-5
Claims 111-133	Supported on: page 2, lines 11-38 page 4, lines 7-22 page 14, lines 10-34 page 15, line 3 to page 16, line 36 page 19, lines 29-32 page 20, lines 33-36 page 27, lines 3-5 page 62, lines 19-20 page 63, lines 15-37 page 68, lines 30-33; page 70, line 31 to page 71, line 11 page 81, lines 19-34 Fig. 10

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 650-326-2400.

Respectfully submitted,



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Attachments
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